

SEQUENCE LISTING

<110> Glaxo Group Limited.

Bonnefoy, Jean-Yves

Ellis, Jonathan H

<120> Antibody.

<130> PG3433

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<150> GB 9809839.5

<151> 1998-05-09

<160> 53

<170> PatentIn Ver. 2.1

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ctg att ttt ttt att gtt ctt tta aaa ggg gtc cag agt gaa gtg aag 95

Leu Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys

20

25

30

Sub AAA

2

ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga tcc atg aaa 143
 Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys
 35 40 45

ctc tcc tgt gta gcc tct gga ttt act ttc agt ggc tac tgg atg tct 191
 Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser
 50 55 60

tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt gct gaa att 239
 Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile
 65 70 75

aga ttg aaa tct gat aat tat gca aca cat tat gcg gag tct gtg aaa 287
 Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys
 80 85 90 95

ggg aag ttc acc atc tca aga gat gat tcc aaa agt cgt ctc tac ctg 335
 Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu
 100 105 110

caa atg aac agc tta aga gct gaa gac agt gga gtt tat tac tgt aca 383
 Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr
 115 120 125

gat ttc ata gac tgg ggc caa ggg aca cta gt 415
 Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu
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ggt cag ttt ctg ggg gtg ctt atg ttc tgg atc tct gga gtc agt ggg	95
Val Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly	
20 25 30	
gat att gtg ata acc cag gat gaa ctc tcc aat cct gtc act tct gga	143
Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly	
35 40 45	
gaa tca gtt tcc atc tcc tgc agg tct agt aag agt ctc ctg tat aag	191
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys	
50 55 60	
gat ggg aag aca tac ttg aat tgg ttt ctg cag aga cca gga caa tct	239
Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser	
65 70 75	
cct cag ctc ctg atg tat ttg atg tcc acc cgt gca tca gga gtc tca	287
Pro Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser	
80 85 90 95	
gac cgg ttt agt ggc agt ggg tca ggc aca gat ttc acc ctg gaa atc	335
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile	
100 105 110	
agt aga gtg aag gct gag gat gtg ggt gtg tat tac tgt caa caa ctt	383
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu	
115 120 125	
gta gag tat cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aaa	431
Val Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys	
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437

Arg Thr

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Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn

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<213> Mus musculus

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<213> Mus musculus

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Gln Gln Leu Val Glu Tyr Pro Phe Thr

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<210> 8

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<222> (1)..(27)

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caa cag ctg gta gag tat cca ttc acg

27

Gln Gln Leu Val Glu Tyr Pro Phe Thr

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<210> 9

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<212> PRT

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Gly Tyr Trp Met Ser

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<210> 10

<211> 15

<212> DNA

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<222> (1)..(15)

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ggc tac tgg atg tcc

15

Gly Tyr Trp Met Ser

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<210> 11

<211> 19

<212> PRT

<213> Mus musculus

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Val Lys Gly

<210> 12

<211> 57

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<221> CDS

<222> (1)..(57)

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Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
1 5 10 15

gtg aag ggg 57
Val Lys Gly

<210> 13

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<210> 15

<211> 19

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
sequence

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Val His Ser

<210> 16

<211> 19

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
sequence

<400> 16

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1 5 10 15

Ala Gln Ala

<210> 17

<211> 348

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Humanised
anti-CD23 antibody light chain variable region

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<221> CDS

<222> (1)..(348)

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1 5 10 15

gag ccg gcc tcc atc tcc tgt cgc tcg agt aag agt ctc ctg tat aag 96
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
 20 25 30

gat ggg aag aca tac ttg aat tgg tac ctg cag aag cca ggg cag tct 144
 Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

cca cag ctc ctg atc tat ttg atg tcc acc cgg gca tca ggg gtc cct 192
 Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
 50 55 60

gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgt caa cag ctg 288
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
 85 90 95

gta gag tat cca ttc acg ttc ggc caa ggg acc aag gtg gag atc aaa 336
 Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

cgt acg gtg gct 348
 Arg Thr Val Ala
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<210> 18

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 anti-CD23 antibody heavy chain variable region.

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<222> (1)..(1335)

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tcc ctt aga ctc tcc tgt gca gct agc gga ttc act ttc agt ggc tac 96

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr

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25

30

tgg atg tcc tgg gtc cgc cag gct cca ggg aag ggg ctc gag tgg gtt 144

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

gct gaa att aga ttg aaa tct gat aat tat gca aca cat tat gcg gag 192

Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu

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55

60

tct gtg aag ggg aaa ttc acc atc tca aga gat gat tca aaa tct aga 240

Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg

65

70

75

80

ctg tat ctg caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat 288

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr

85

90

95

tac tgt aca gat ttc ata gac tgg ggc cag gga aca cta gtc acc gtc 336

Tyr Cys Thr Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu Val Thr Val

100

105

110

tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc 384

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser

115

120

125

11

tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag	432
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
130 135 140	
gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg	480
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
145 150 155 160	
acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc	528
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
165 170 175	
tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc	576
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
180 185 190	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg	624
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
195 200 205	
gac aag aaa gtg gag ccc aaa tct tgt gac aaa act cac aca tgc cca	672
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
210 215 220	
ccg tgc cca gca cct gaa ctc gcg ggg gca ccg tca gtc ttc ctc ttc	720
Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe	
225 230 235 240	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	768
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
245 250 255	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	816
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
260 265 270	

12

aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg 864
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285

cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc 912
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300

gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc 960
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320

tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc 1008
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335

aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg 1056
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 340 345 350

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc 1104
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 355 360 365

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg 1152
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 370 375 380

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc 1200
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 385 390 395 400

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 1248
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 405 410 415

13

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 1296
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1335
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 19

<211> 57

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 19

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<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 20

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<210> 21

<211> 57

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 21

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<210> 22

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 22

gatgcgtacg tytkatytcc avcttkgt 28

<210> 23

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 23

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<210> 24

<211> 63

<212> DNA

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<223> Description of Artificial Sequence: Oligo

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<210> 25

<211> 63

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

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aag 63

<210> 26

<211> 36

<212> DNA

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<223> Description of Artificial Sequence: Oligo

<400> 26

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<210> 27

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 27

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

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cagctgttga cagtaataaa cccc 84

<210> 29

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 29

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<210> 30

<211> 66

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

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cgccat 66

<210> 31

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

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<210> 32

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

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<210> 33

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 33

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<210> 34

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 34

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<210> 35

<211> 66

<212> DNA

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<223> Description of Artificial Sequence: Oligo

<400> 35

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<210> 36

<211> 69

<212> DNA

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<223> Description of Artificial Sequence: Oligo

<400> 36

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<210> 37

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 37

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<210> 38

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 38

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<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

<400> 39

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<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

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<210> 41

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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37

<210> 42

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
sequence

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<210> 43

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
sequence

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<210> 44

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
sequence

<400> 44

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<210> 45

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
sequence

<400> 45

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<210> 46

<211> 415

<212> DNA

<213> Mus musculus

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aacttccctt tcacagactc cgcataatgt gttgcataat tatcagattt caatctaatt 180
tcagcaaccc actcaagccc cttctctgga gactggcgga cccaagacat ccagtagcca 240
ctgaaagtaa atccagaggc tacacaggag agtttcatgg atcctccagg ttgcaccaag 300
cctcctccag actcctcaag cttcacttca ctctggaccc cttttaaaag aacaataaaa 360
aaaatcagcc caaatccat ggtgaggtcc tgtgtgctga gtaactgtaa agctt 415

<210> 47

<211> 437

<212> DNA

<213> Mus musculus

<400> 47

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tgtgcctgac ccaactgccac taaaccgggc tgagactcct gatgcacggg tggacatcaa 180
atacatcagg agctgaggag attgtcctgg tctctgcaga aaccaattca agtatgtcct 240
cccacctta tacaggagac tcttactaga cctgcaggag atggaaactg attctccaga 300
agtgacagga ttggagagtt catcctgggt tatcacaata tccccactga ctccagagat 360
ccagaacata agcaccccca gaaactgaac agagaacctc atggtgaggt cctgtgtgct 420
gagtaactgt aaagctt                                     437
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<210> 48

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Humanised
anti-CD23 antibody light chain variable region

<400> 48

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aaaatctgtg cctgatccac tgccactgaa cctgtcaggg acccctgatg cccgggtgga 180
catcaaatag atcaggagct gtggagactg ccctggcttc tgcaggatcc aattcaagta 240
tgtcttccca tccttatata ggagactctt actcgagcga caggagatgg aggccggctc 300
tccaggggtg acgggcaggg agagtggaga ctgagtcac acaatatc 348
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<211> 1335

<212> DNA

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<223> Description of Artificial Sequence: Humanised

anti-CD23 antibody heavy chain variable region

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catcacggag catgagaaga cggtcccttg ctgccacctg ctcttgcca cggtgagctt 120
gctgtagagg aagaaggagc cgtcggagtc cagcacggga ggcgtggtct tgtagttgtt 180
ctccggctgc ccattgctct cccactccac ggcgatgtcg ctgggataga agcctttgac 240
caggcaggtc aggctgacct ggttcttggt cagctcatcc cgggatgggg gcagggtgta 300
cacctgtggt tctcggggct gccctttggc tttggagatg gttttctcga tgggggctgg 360
gagggctttg ttggagacct tgcacttgta ctcttgcca ttcagccagt cctggtgcag 420
gacggtgagg acgctgacca caggtacgt gctgtgtgac tgctcctccc gcggctttgt 480
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<210> 50

<211> 137

<212> PRT

<213> Mus musculus

<400> 50

Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Asp Phe Gly Leu

1

5

10

15

24

Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys Leu
 20 25 30

Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu
 35 40 45

Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser Trp
 50 55 60

Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg
 65 70 75 80

Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys Gly
 85 90 95

Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu Gln
 100 105 110

Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr Asp
 115 120 125

Phe Ile Asp Trp Gly Gln Gly Thr Leu
 130 135

<210> 51

<211> 145

<212> PRT

<213> Mus musculus

<400> 51

Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Arg Phe Ser Val
 1 5 10 15

Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly Asp
 20 25 30

Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly Glu
 35 40 45

25

Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp
 50 55 60

Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro
 65 70 75 80

Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser Asp
 85 90 95

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile Ser
 100 105 110

Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu Val
 115 120 125

Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
 130 135 140

Thr

145

<210> 52

<211> 116

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Humanised
 anti-CD23 antibody light chain variable region

<400> 52

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

26

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
 85 90 95

Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

Arg Thr Val Ala
 115

<210> 53

<211> 444

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Humanised
 anti-CD23 antibody heavy chain variable region.

<400> 53

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
 20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
 50 55 60

Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg
 65 70 75 80

27

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
165 170 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

28

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440